



SEQUENCE LISTING

<110> Meyers, Rachel
Cook, William James
Williamson, Mark
Rudolph-Owen, Laura A.
Gimeno, Ruth

<120> 21481, A NOVEL DEHYDROGENASE MOLECULE
AND USES THEREFOR

<130> MPI00-079P1RCP2CN1M

<140> 10/664,506

<141> 2003-09-17

<150> 09/838,561

<151> 2001-04-18

<150> 09/816,760

<151> 2001-03-23

<150> 09/634,955

<151> 2000-08-08

<150> 60/192,002

<151> 2000-03-24

<160> 34

<170> FastSEQ for Windows Version 4.0

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Met Ala Ala Thr Arg Ala Gly Pro Arg Ala Arg Glu Ile Phe Thr
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tcg ctg gag tac gga ccg gtg ccg gag agc cac gca tgc gca ctg gcc 155
Ser Leu Glu Tyr Gly Pro Val Pro Glu Ser His Ala Cys Ala Leu Ala
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tgg ctg gac acc cag gac cgg tgc ttg ggc cac tat gtg aat ggg aag 203
Trp Leu Asp Thr Gln Asp Arg Cys Leu Gly His Tyr Val Asn Gly Lys
35 40 45

tgg tta aag cct gaa cac aga aat tca gtg cct tgc cag gat ccc atc 251
Trp Leu Lys Pro Glu His Arg Asn Ser Val Pro Cys Gln Asp Pro Ile
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aca gga gag aac ttg gcc agt tgc ctg cag gca cag gcc gag gat gtg	299
Thr Gly Glu Asn Leu Ala Ser Cys Leu Gln Ala Gln Ala Glu Asp Val	
65 70 75	
gct gca gcc gtg gag gca gcc agg atg gca ttt aag ggc tgg agt gcg	347
Ala Ala Ala Val Glu Ala Ala Arg Met Ala Phe Lys Gly Trp Ser Ala	
80 85 90 95	
cac ccc ggc gtc gtc cgg gcc cag cac ctg acc agg ctg gcc gag gtg	395
His Pro Gly Val Val Arg Ala Gln His Leu Thr Arg Leu Ala Glu Val	
100 105 110	
atc cag aag cac cag cgg ctg ctg tgg acc ctg gaa tcc ctg gtg act	443
Ile Gln Lys His Gln Arg Leu Leu Trp Thr Leu Glu Ser Leu Val Thr	
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Gly Arg Ala Val Arg Glu Val Arg Asp Gly Asp Val Gln Leu Ala Gln	
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cag ctg ctc cac tac cat gca atc cag gca tcc acc cag gag gag gca	539
Gln Leu Leu His Tyr His Ala Ile Gln Ala Ser Thr Gln Glu Glu Ala	
145 150 155	
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Leu Ala Gly Trp Glu Pro Met Gly Val Ile Gly Leu Ile Leu Pro Pro	
160 165 170 175	
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Thr Phe Ser Phe Leu Glu Met Met Trp Arg Ile Cys Pro Ala Leu Ala	
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gtg ggc tgc acc gtg gtg gcc ctc gtg ccc ccg gcc tcc ccg gcg ccc	683
Val Gly Cys Thr Val Val Ala Leu Val Pro Pro Ala Ser Pro Ala Pro	
195 200 205	
ctc ctc ctg gcc cag ctg gcg ggg gag ctg ggc ccc ttc ccg gga atc	731
Leu Leu Leu Ala Gln Leu Ala Gly Glu Leu Gly Pro Phe Pro Gly Ile	
210 215 220	
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Leu Asn Val Val Ser Gly Pro Ala Ser Leu Val Pro Ile Leu Ala Ser	
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Gln Pro Gly Ile Arg Lys Val Ala Phe Cys Gly Ala Pro Glu Glu Gly	
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Arg Ala Leu Arg Arg Ser Leu Ala Gly Glu Cys Ala Glu Leu Gly Leu	
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Asp Ser Ala Val Glu Gly Val Val Asp Ala Ala Trp Ser Asp Arg Gly	
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Pro Gly Gly Leu Arg Leu Leu Ile Gln Glu Ser Val Trp Asp Glu Ala	
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320 325 330 335	
ctg gat ggg gcc gtg gac atg ggg gcc cgg ggg gct gcc gca tgt gac	1115
Leu Asp Gly Ala Val Asp Met Gly Ala Arg Gly Ala Ala Ala Cys Asp	
340 345 350	
ctg gtc cag cgc ttt gtg cgt gag gcc cag agc cag ggt gca cag gtg	1163
Leu Val Gln Arg Phe Val Arg Glu Ala Gln Ser Gln Gly Ala Gln Val	
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ttc cag gct ggt gat gtg cct tct gaa cgc cca ttc tat ccc cca acc	1211
Phe Gln Ala Gly Asp Val Pro Ser Glu Arg Pro Phe Tyr Pro Pro Thr	
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ttg gtc tcc aac ctg ccc cca gcc tcc cca tgt gcc cag gtg gag gtg	1259
Leu Val Ser Asn Leu Pro Pro Ala Ser Pro Cys Ala Gln Val Glu Val	
385 390 395	
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Pro Trp Pro Val Val Val Ala Ser Pro Phe Arg Thr Ala Lys Glu Ala	
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ctg ttg gtg gcc aac ggg acg ccc cgc ggg ggc agc gcc agt gtg tgg	1355
Leu Leu Val Ala Asn Gly Thr Pro Arg Gly Gly Ser Ala Ser Val Trp	
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Ser Glu Arg Leu Gly Gln Ala Leu Glu Leu Gly Tyr Gly Leu Gln Val	
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Gly Thr Val Trp Ile Asn Ala His Gly Leu Arg Asp Pro Ser Val Pro	
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Thr Gly Gly Cys Lys Glu Ser Gly Cys Ser Trp His Gly Gly Pro Asp	
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Gly Leu Tyr Glu Tyr Leu Arg Pro Ser Gly Thr Pro Ala Arg Leu Ser	
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tgc ctc tcc aag aac ctg aac tat gac acc ttt ggc ctc gct gtg ccc	1595
Cys Leu Ser Lys Asn Leu Asn Tyr Asp Thr Phe Gly Leu Ala Val Pro	
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tca acc ctg ccg gct ggg cct gaa ata ggg ccc agc cca gca ccc ccc	1643
Ser Thr Leu Pro Ala Gly Pro Glu Ile Gly Pro Ser Pro Ala Pro Pro	
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tat ggg ctc ttc gtt ggg ggc cgt ttc cag gct cct ggg gcc cga agc	1691
Tyr Gly Leu Phe Val Gly Gly Arg Phe Gln Ala Pro Gly Ala Arg Ser	
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tcc agg ccc atc cgg gat tct tct ggc aat ctc cat ggc tac gtg gct	1739
Ser Arg Pro Ile Arg Asp Ser Ser Gly Asn Leu His Gly Tyr Val Ala	
545 550 555	
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Glu Gly Gly Ala Lys Asp Ile Arg Gly Ala Val Glu Ala Ala His Gln	
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Leu Trp Ala Leu Ala Ala Ala Leu Glu Arg Arg Lys Ser Thr Leu Ala	
595 600 605	
tca agg ctg gag agg cag gga gcg gag ctc aag gct gcg gag gcg gag	1931
Ser Arg Leu Glu Arg Gln Gly Ala Glu Leu Lys Ala Ala Glu Ala Glu	
610 615 620	
gtg gag ctg agc gca aga cga ctt cgg gcg tgg ggg gcc cgg gtg cag	1979
Val Glu Leu Ser Ala Arg Arg Leu Arg Ala Trp Gly Ala Arg Val Gln	
625 630 635	
gcc caa ggc cac acc ctg cag gta gcc ggg ctg aga ggc cct gtg ctg	2027
Ala Gln Gly His Thr Leu Gln Val Ala Gly Leu Arg Gly Pro Val Leu	
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cgc ctg cgg gag ccg ctg ggt gtg ctg gct gtg gtg tgt ccg gac gag	2075
Arg Leu Arg Glu Pro Leu Gly Val Leu Ala Val Val Cys Pro Asp Glu	
660 665 670	
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Trp Pro Leu Leu Ala Phe Val Ser Leu Leu Ala Pro Ala Leu Ala Tyr	
675 680 685	
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Gly Asn Thr Val Val Met Val Pro Ser Ala Ala Cys Pro Leu Leu Ala	
690 695 700	
ctg gag gtc tgc cag gac atg gcc acc gtg ttc cca gca ggc ctg gcc	2219
Leu Glu Val Cys Gln Asp Met Ala Thr Val Phe Pro Ala Gly Leu Ala	
705 710 715	
aac gtg gtg aca gga gac cgg gac cat ctg acc cgc tgc ctg gcc ttg	2267
Asn Val Val Thr Gly Asp Arg Asp His Leu Thr Arg Cys Leu Ala Leu	
720 725 730 735	
cac caa gac gtc cag gcc atg tgg tat ttc gga tca gcc cag ggt tcc	2315
His Gln Asp Val Gln Ala Met Trp Tyr Phe Gly Ser Ala Gln Gly Ser	
740 745 750	
cag ttt gtc gag tgg gcc tcg gca gga aac ctc aaa ccg gtg tgg gcg	2363
Gln Phe Val Glu Trp Ala Ser Ala Gly Asn Leu Lys Pro Val Trp Ala	
755 760 765	
agc agg ggc tgc ccg cgg gcc tgg gac cag gag gcc gag ggg gca ggc	2411
Ser Arg Gly Cys Pro Arg Ala Trp Asp Gln Glu Ala Glu Gly Ala Gly	
770 775 780	
cca gag ctg ggg ctg cga gtg gcg cgg acc aag gcc ctg tgg ctg cct	2459
Pro Glu Leu Gly Leu Arg Val Ala Arg Thr Lys Ala Leu Trp Leu Pro	
785 790 795	
atg ggg gac tgatgacctga gcgccacct ctgcattttg gacacctcac	2508
Met Gly Asp	
800	
accaagggga gatgcacccc acagacacct gggactttcc ccttctgggt cctgtgtctc	2568
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 Leu Asp Thr Gln Asp Arg Cys Leu Gly His Tyr Val Asn Gly Lys Trp
 35 40 45
 Leu Lys Pro Glu His Arg Asn Ser Val Pro Cys Gln Asp Pro Ile Thr
 50 55 60
 Gly Glu Asn Leu Ala Ser Cys Leu Gln Ala Gln Ala Glu Asp Val Ala
 65 70 75 80
 Ala Ala Val Glu Ala Ala Arg Met Ala Phe Lys Gly Trp Ser Ala His
 85 90 95
 Pro Gly Val Val Arg Ala Gln His Leu Thr Arg Leu Ala Glu Val Ile
 100 105 110
 Gln Lys His Gln Arg Leu Leu Trp Thr Leu Glu Ser Leu Val Thr Gly
 115 120 125
 Arg Ala Val Arg Glu Val Arg Asp Gly Asp Val Gln Leu Ala Gln Gln
 130 135 140
 Leu Leu His Tyr His Ala Ile Gln Ala Ser Thr Gln Glu Glu Ala Leu
 145 150 155 160
 Ala Gly Trp Glu Pro Met Gly Val Ile Gly Leu Ile Leu Pro Pro Thr
 165 170 175
 Phe Ser Phe Leu Glu Met Met Trp Arg Ile Cys Pro Ala Leu Ala Val
 180 185 190
 Gly Cys Thr Val Val Ala Leu Val Pro Pro Ala Ser Pro Ala Pro Leu
 195 200 205
 Leu Leu Ala Gln Leu Ala Gly Glu Leu Gly Pro Phe Pro Gly Ile Leu
 210 215 220
 Asn Val Val Ser Gly Pro Ala Ser Leu Val Pro Ile Leu Ala Ser Gln
 225 230 235 240
 Pro Gly Ile Arg Lys Val Ala Phe Cys Gly Ala Pro Glu Glu Gly Arg
 245 250 255
 Ala Leu Arg Arg Ser Leu Ala Gly Glu Cys Ala Glu Leu Gly Leu Ala
 260 265 270
 Leu Gly Thr Glu Ser Leu Leu Leu Thr Asp Thr Ala Asp Val Asp
 275 280 285
 Ser Ala Val Glu Gly Val Val Asp Ala Ala Trp Ser Asp Arg Gly Pro
 290 295 300
 Gly Gly Leu Arg Leu Leu Ile Gln Glu Ser Val Trp Asp Glu Ala Met
 305 310 315 320
 Arg Arg Leu Gln Glu Arg Met Gly Arg Leu Arg Ser Gly Arg Gly Leu
 325 330 335
 Asp Gly Ala Val Asp Met Gly Ala Arg Gly Ala Ala Ala Cys Asp Leu
 340 345 350
 Val Gln Arg Phe Val Arg Glu Ala Gln Ser Gln Gly Ala Gln Val Phe
 355 360 365
 Gln Ala Gly Asp Val Pro Ser Glu Arg Pro Phe Tyr Pro Pro Thr Leu
 370 375 380
 Val Ser Asn Leu Pro Pro Ala Ser Pro Cys Ala Gln Val Glu Val Pro
 385 390 395 400
 Trp Pro Val Val Val Ala Ser Pro Phe Arg Thr Ala Lys Glu Ala Leu
 405 410 415
 Leu Val Ala Asn Gly Thr Pro Arg Gly Gly Ser Ala Ser Val Trp Ser
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 Glu Arg Leu Gly Gln Ala Leu Glu Gly Tyr Gly Leu Gln Val Gly
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 Thr Val Trp Ile Asn Ala His Gly Leu Arg Asp Pro Ser Val Pro Thr

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1				5					10					15					
ctg	gag	tac	gga	ccg	gtg	ccg	gag	agc	cac	gca	tgc	gca	ctg	gcc	tgg				96
Leu	Glu	Tyr	Gly	Pro	Val	Pro	Glu	Ser	His	Ala	Cys	Ala	Leu	Ala	Trp				
			20					25					30						

ctg gac acc cag gac cgg tgc ttg ggc cac tat gtg aat ggg aag tgg	144
Leu Asp Thr Gln Asp Arg Cys Leu Gly His Tyr Val Asn Gly Lys Trp	
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tta aag cct gaa cac aga aat tca gtg cct tgc cag gat ccc atc aca	192
Leu Lys Pro Glu His Arg Asn Ser Val Pro Cys Gln Asp Pro Ile Thr	
50 55 60	
gga gag aac ttg gcc agt tgc ctg cag gca cag gcc gag gat gtg gct	240
Gly Glu Asn Leu Ala Ser Cys Leu Gln Ala Gln Ala Glu Asp Val Ala	
65 70 75 80	
gca gcc gtg gag gca gcc agg atg gca ttt aag ggc tgg agt gcg cac	288
Ala Ala Val Glu Ala Ala Arg Met Ala Phe Lys Gly Trp Ser Ala His	
85 90 95	
ccc ggc gtc gtc cgg gcc cag cac ctg acc agg ctg gcc gag gtg atc	336
Pro Gly Val Val Arg Ala Gln His Leu Thr Arg Leu Ala Glu Val Ile	
100 105 110	
cag aag cac cag cgg ctg ctg tgg acc ctg gaa tcc ctg gtg act ggg	384
Gln Lys His Gln Arg Leu Leu Trp Thr Leu Glu Ser Leu Val Thr Gly	
115 120 125	
cgg gct gtt cga gag gtt cga gac ggg gac gtc cag ctg gcc cag cag	432
Arg Ala Val Arg Glu Val Arg Asp Gly Asp Val Gln Leu Ala Gln Gln	
130 135 140	
ctg ctc cac tac cat gca atc cag gca tcc acc cag gag gag gca ctg	480
Leu Leu His Tyr His Ala Ile Gln Ala Ser Thr Gln Glu Glu Ala Leu	
145 150 155 160	
gca ggc tgg gag ccc atg gga gta att ggc ctc atc ctg cca ccc aca	528
Ala Gly Trp Glu Pro Met Gly Val Ile Gly Leu Ile Leu Pro Pro Thr	
165 170 175	
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Phe Ser Phe Leu Glu Met Met Trp Arg Ile Cys Pro Ala Leu Ala Val	
180 185 190	
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Gly Cys Thr Val Val Ala Leu Val Pro Pro Ala Ser Pro Ala Pro Leu	
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Leu Leu Ala Gln Leu Ala Gly Glu Leu Gly Pro Phe Pro Gly Ile Leu	
210 215 220	
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Asn Val Val Ser Gly Pro Ala Ser Leu Val Pro Ile Leu Ala Ser Gln	
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Pro Gly Ile Arg Lys Val Ala Phe Cys Gly Ala Pro Glu Glu Gly Arg	
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gcc ctt cga cgg agc ctg gcg gga gag tgt gcg gag ctg ggc ctg gcg	816
Ala Leu Arg Arg Ser Leu Ala Gly Glu Cys Ala Glu Leu Gly Leu Ala	
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275 280 285	

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Ser Ala Val Glu Gly Val Val Asp Ala Ala Trp Ser Asp Arg Gly Pro	
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Gly Gly Leu Arg Leu Leu Ile Gln Glu Ser Val Trp Asp Glu Ala Met	
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aga cgg ctg cag gag cgg atg ggg cgg ctt cgg agt ggc cga ggg ctg	1008
Arg Arg Leu Gln Glu Arg Met Gly Arg Leu Arg Ser Gly Arg Gly Leu	
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gat ggg gcc gtg gac atg ggg gcc cgg ggg gct gcc gca tgt gac ctg	1056
Asp Gly Ala Val Asp Met Gly Ala Arg Gly Ala Ala Cys Asp Leu	
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Val Gln Arg Phe Val Arg Glu Ala Gln Ser Gln Gly Ala Gln Val Phe	
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Gln Ala Gly Asp Val Pro Ser Glu Arg Pro Phe Tyr Pro Pro Thr Leu	
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Trp Pro Val Val Val Ala Ser Pro Phe Arg Thr Ala Lys Glu Ala Leu	
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Thr Val Trp Ile Asn Ala His Gly Leu Arg Asp Pro Ser Val Pro Thr	
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Gly Gly Cys Lys Glu Ser Gly Cys Ser Trp His Gly Gly Pro Asp Gly	
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ctg tat gag tat ctg cgg ccc tca ggg acc cct gcc cgg ctg tcc tgc	1488
Leu Tyr Glu Tyr Leu Arg Pro Ser Gly Thr Pro Ala Arg Leu Ser Cys	
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Leu Ser Lys Asn Leu Asn Tyr Asp Thr Phe Gly Leu Ala Val Pro Ser	
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acc ctg ccg gct ggg cct gaa ata ggg ccc agc cca gca ccc ccc tat	1584
Thr Leu Pro Ala Gly Pro Glu Ile Gly Pro Ser Pro Ala Pro Pro Tyr	
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Gly Leu Phe Val Gly Gly Arg Phe Gln Ala Pro Gly Ala Arg Ser Ser	
530 535 540	

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Arg Pro Ile Arg Asp Ser Ser Gly Asn Leu His Gly Tyr Val Ala Glu	
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Gly Gly Ala Lys Asp Ile Arg Gly Ala Val Glu Ala Ala His Gln Ala	
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Phe Pro Gly Trp Ala Gly Gln Ser Pro Gly Ala Arg Ala Ala Leu Leu	
580 585 590	
tgg gcc ctg gcg gct gca ctg gag cgc cgg aag tct acc ctg gcc tca	1824
Trp Ala Leu Ala Ala Leu Glu Arg Arg Lys Ser Thr Leu Ala Ser	
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Arg Leu Glu Arg Gln Gly Ala Glu Leu Lys Ala Ala Glu Ala Glu Val	
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Glu Leu Ser Ala Arg Arg Leu Arg Ala Trp Gly Ala Arg Val Gln Ala	
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Gln Gly His Thr Leu Gln Val Ala Gly Leu Arg Gly Pro Val Leu Arg	
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Leu Arg Glu Pro Leu Gly Val Leu Ala Val Val Cys Pro Asp Glu Trp	
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Asn Thr Val Val Met Val Pro Ser Ala Ala Cys Pro Leu Leu Ala Leu	
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Glu Val Cys Gln Asp Met Ala Thr Val Phe Pro Ala Gly Leu Ala Asn	
705 710 715 720	
gtg gtg aca gga gac cgg gac cat ctg acc cgc tgc ctg gcc ttg cac	2208
Val Val Thr Gly Asp Arg Asp His Leu Thr Arg Cys Leu Ala Leu His	
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caa gac gtc cag gcc atg tgg tat ttc gga tca gcc cag ggt tcc cag	2256
Gln Asp Val Gln Ala Met Trp Tyr Phe Gly Ser Ala Gln Gly Ser Gln	
740 745 750	
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Phe Val Glu Trp Ala Ser Ala Gly Asn Leu Lys Pro Val Trp Ala Ser	
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Arg Gly Cys Pro Arg Ala Trp Asp Gln Glu Ala Glu Gly Ala Gly Pro	
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gag ctg ggg ctg cga gtg gcg cgg acc aag gcc ctg tgg ctg cct atg	2400
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ggg gac
Gly Asp

2406

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<222> (331)...(1263)

<221> misc_feature
<222> 1337
<223> n = A,T,C or G

<400> 4
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cttccaaaaa tgcagaccca ttttaattaa gtttgtaatt aaccactggg gagggcaggc 120
cccctggatt cggctctgctt tcggagacac tgtgagtaac ttcctatttg ttgaacattt 180
ggggattagc acgcccactg ggtgttcagc ttggaggctt gcacagagct gagctccctg 240
cagccttggg cctccccctg ccctgggagt cctgatcagc gtctctttgc aaagccaatc 300
cccttttact ccgttgtccc ccagaacaag atg gga gtc atg gcc atg ctg atg 354
Met Gly Val Met Ala Met Leu Met
1 5

ctc ccc ctg ctg ctg ctg gga atc agc ggc ctc ctc ttc att tac caa 402
Leu Pro Leu Leu Leu Leu Gly Ile Ser Gly Leu Leu Phe Ile Tyr Gln
10 15 20

gag gtg tcc agg ctg tgg tca aag tca gct gtg cag aac aaa gtg gtg 450
Glu Val Ser Arg Leu Trp Ser Lys Ser Ala Val Gln Asn Lys Val Val
25 30 35 40

gtg atc acc gat gcc atc tca gga ctg ggc aag gag tgt gct cgg gtg 498
Val Ile Thr Asp Ala Ile Ser Gly Leu Gly Lys Glu Cys Ala Arg Val
45 50 55

ttc cac aca ggt ggg gca agg ctg gtg ctg tgt gga aag aac tgg gag 546
Phe His Thr Gly Gly Ala Arg Leu Val Leu Cys Gly Lys Asn Trp Glu
60 65 70

agg cta gag aac cta tat gat gcc ttg atc agc gtg gct gac ccc agc 594
Arg Leu Glu Asn Leu Tyr Asp Ala Leu Ile Ser Val Ala Asp Pro Ser
75 80 85

aag aca ttc acc cca aag ctg gtc ctg ttg gac ctc tca gac atc agc 642
Lys Thr Phe Thr Pro Lys Leu Val Leu Leu Asp Leu Ser Asp Ile Ser
90 95 100

tgt gtc cca gat gtg gca aaa gaa gtc ctg gat tgc tat ggc tgt gtg 690
Cys Val Pro Asp Val Ala Lys Glu Val Leu Asp Cys Tyr Gly Cys Val
105 110 115 120

gac atc ctc atc aac aat gcc agt gtg aag gtg aag ggg cct gcc cat 738
Asp Ile Leu Ile Asn Asn Ala Ser Val Lys Val Lys Gly Pro Ala His
125 130 135

aag att tct ctg gag ctc gac aaa aag atc atg gat gcc aat tac ttt 786
Lys Ile Ser Leu Glu Leu Asp Lys Lys Ile Met Asp Ala Asn Tyr Phe
140 145 150

ggc ccc atc aca ttg acg aaa gcc ctg ctt ccc aac atg atc tcc cgg 834
 Gly Pro Ile Thr Leu Thr Lys Ala Leu Leu Pro Asn Met Ile Ser Arg
 155 160 165

aga aca ggc caa atc gtg tta gtg aat aat atc caa ggg aag ttt gga 882
 Arg Thr Gly Gln Ile Val Leu Val Asn Asn Ile Gln Gly Lys Phe Gly
 170 175 180

atc ccg ttc cgt acg act tac gct gcc tcc aag cac gca gcc ctg ggc 930
 Ile Pro Phe Arg Thr Thr Tyr Ala Ala Ser Lys His Ala Ala Leu Gly
 185 190 195 200

ttc ttt gac tgc ctc cga gcc gaa gtg gag gaa tac gat gtt gtc atc 978
 Phe Phe Asp Cys Leu Arg Ala Glu Val Glu Glu Tyr Asp Val Val Ile
 205 210 215

agc acc gtg agc ccg act ttc atc cgg tcg tac cac gtg tat cca gag 1026
 Ser Thr Val Ser Pro Thr Phe Ile Arg Ser Tyr His Val Tyr Pro Glu
 220 225 230

caa gga aac tgg gaa gct tcc att tgg aaa ttc ttt ttc agg aag ctg 1074
 Gln Gly Asn Trp Glu Ala Ser Ile Trp Lys Phe Phe Phe Arg Lys Leu
 235 240 245

acc tac ggc gtg cac cca gta gag gtg gcg gag gag gtg atg cgc acc 1122
 Thr Tyr Gly Val His Pro Val Glu Val Ala Glu Glu Val Met Arg Thr
 250 255 260

gtg cgg agg aag aag caa gag gtg ttt atg gcc aac ccc atc ccc aag 1170
 Val Arg Arg Lys Lys Gln Glu Val Phe Met Ala Asn Pro Ile Pro Lys
 265 270 275 280

gcc gcc gtg tac gtc cgc acc ttc ttc ccg gag ttc ttt ttc gcc gtg 1218
 Ala Ala Val Tyr Val Arg Thr Phe Phe Pro Glu Phe Phe Phe Ala Val
 285 290 295

gtg gcc tgt ggg gtg aag gag aag ctc aat gtc ccg gag gag ggg 1263
 Val Ala Cys Gly Val Lys Glu Lys Leu Asn Val Pro Glu Glu Gly
 300 305 310

taactgcagg aggccaaatg ggccaccctc tggaataaaa ggtttttctg gcaaaaaaaaa 1323
 aaaaaaaaaa aaantttgcg gccgcaagct tattcccttt agggagggtt aatttt 1379

<210> 5
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 5
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 1 5 10 15
 Ser Gly Leu Leu Phe Ile Tyr Gln Glu Val Ser Arg Leu Trp Ser Lys
 20 25 30
 Ser Ala Val Gln Asn Lys Val Val Ile Thr Asp Ala Ile Ser Gly
 35 40 45
 Leu Gly Lys Glu Cys Ala Arg Val Phe His Thr Gly Gly Ala Arg Leu
 50 55 60
 Val Leu Cys Gly Lys Asn Trp Glu Arg Leu Glu Asn Leu Tyr Asp Ala
 65 70 75 80
 Leu Ile Ser Val Ala Asp Pro Ser Lys Thr Phe Thr Pro Lys Leu Val
 85 90 95
 Leu Leu Asp Leu Ser Asp Ile Ser Cys Val Pro Asp Val Ala Lys Glu
 100 105 110

Val	Leu	Asp	Cys	Tyr	Gly	Cys	Val	Asp	Ile	Leu	Ile	Asn	Asn	Ala	Ser
	115						120					125			
Val	Lys	Val	Lys	Gly	Pro	Ala	His	Lys	Ile	Ser	Leu	Glu	Leu	Asp	Lys
	130					135					140				
Lys	Ile	Met	Asp	Ala	Asn	Tyr	Phe	Gly	Pro	Ile	Thr	Leu	Thr	Lys	Ala
	145				150					155					160
Leu	Leu	Pro	Asn	Met	Ile	Ser	Arg	Arg	Thr	Gly	Gln	Ile	Val	Leu	Val
			165						170					175	
Asn	Asn	Ile	Gln	Gly	Lys	Phe	Gly	Ile	Pro	Phe	Arg	Thr	Thr	Tyr	Ala
		180						185					190		
Ala	Ser	Lys	His	Ala	Ala	Leu	Gly	Phe	Phe	Asp	Cys	Leu	Arg	Ala	Glu
	195						200					205			
Val	Glu	Glu	Tyr	Asp	Val	Val	Ile	Ser	Thr	Val	Ser	Pro	Thr	Phe	Ile
	210					215					220				
Arg	Ser	Tyr	His	Val	Tyr	Pro	Glu	Gln	Gly	Asn	Trp	Glu	Ala	Ser	Ile
	225				230					235					240
Trp	Lys	Phe	Phe	Phe	Arg	Lys	Leu	Thr	Tyr	Gly	Val	His	Pro	Val	Glu
			245						250					255	
Val	Ala	Glu	Glu	Val	Met	Arg	Thr	Val	Arg	Arg	Lys	Lys	Gln	Glu	Val
			260					265					270		
Phe	Met	Ala	Asn	Pro	Ile	Pro	Lys	Ala	Ala	Val	Tyr	Val	Arg	Thr	Phe
	275						280					285			
Phe	Pro	Glu	Phe	Phe	Phe	Ala	Val	Val	Ala	Cys	Gly	Val	Lys	Glu	Lys
	290					295					300				
Leu	Asn	Val	Pro	Glu	Glu	Gly									
	305				310										

<210> 6
 <211> 933
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(933)

<400> 6																
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Met	Gly	Val	Met	Ala	Met	Leu	Met	Leu	Pro	Leu	Leu	Leu	Leu	Gly	Ile	
1				5					10					15		
agc ggc ctc ctc ttc att tac caa gag gtg tcc agg ctg tgg tca aag															96	
Ser	Gly	Leu	Leu	Phe	Ile	Tyr	Gln	Glu	Val	Ser	Arg	Leu	Trp	Ser	Lys	
			20					25					30			
tca gct gtg cag aac aaa gtg gtg gtg atc acc gat gcc atc tca gga															144	
Ser	Ala	Val	Gln	Asn	Lys	Val	Val	Val	Ile	Thr	Asp	Ala	Ile	Ser	Gly	
		35					40					45				
ctg ggc aag gag tgt gct cgg gtg ttc cac aca ggt ggg gca agg ctg															192	
Leu	Gly	Lys	Glu	Cys	Ala	Arg	Val	Phe	His	Thr	Gly	Gly	Ala	Arg	Leu	
	50					55					60					
gtg ctg tgt gga aag aac tgg gag agg cta gag aac cta tat gat gcc															240	
Val	Leu	Cys	Gly	Lys	Asn	Trp	Glu	Arg	Leu	Glu	Asn	Leu	Tyr	Asp	Ala	
	65				70				75					80		
ttg atc agc gtg gct gac ccc agc aag aca ttc acc cca aag ctg gtc															288	
Leu	Ile	Ser	Val	Ala	Asp	Pro	Ser	Lys	Thr	Phe	Thr	Pro	Lys	Leu	Val	
				85					90					95		
ctg ttg gac ctc tca gac atc agc tgt gtc cca gat gtg gca aaa gaa															336	
Leu	Leu	Asp	Leu	Ser	Asp	Ile	Ser	Cys	Val	Pro	Asp	Val	Ala	Lys	Glu	

100					105					110						
gtc	ctg	gat	tgc	tat	ggc	tgt	gtg	gac	atc	ctc	atc	aac	aat	gcc	agt	384
Val	Leu	Asp	Cys	Tyr	Gly	Cys	Val	Asp	Ile	Leu	Ile	Asn	Asn	Ala	Ser	
		115						120					125			
gtg	aag	gtg	aag	ggg	cct	gcc	cat	aag	att	tct	ctg	gag	ctc	gac	aaa	432
Val	Lys	Val	Lys	Gly	Pro	Ala	His	Lys	Ile	Ser	Leu	Glu	Leu	Asp	Lys	
	130					135					140					
aag	atc	atg	gat	gcc	aat	tac	ttt	ggc	ccc	atc	aca	ttg	acg	aaa	gcc	480
Lys	Ile	Met	Asp	Ala	Asn	Tyr	Phe	Gly	Pro	Ile	Thr	Leu	Thr	Lys	Ala	
145					150					155					160	
ctg	ctt	ccc	aac	atg	atc	tcc	cgg	aga	aca	ggc	caa	atc	gtg	tta	gtg	528
Leu	Leu	Pro	Asn	Met	Ile	Ser	Arg	Arg	Thr	Gly	Gln	Ile	Val	Leu	Val	
				165					170					175		
aat	aat	atc	caa	ggg	aag	ttt	gga	atc	ccg	ttc	cgt	acg	act	tac	gct	576
Asn	Asn	Ile	Gln	Gly	Lys	Phe	Gly	Ile	Pro	Phe	Arg	Thr	Thr	Tyr	Ala	
			180					185					190			
gcc	tcc	aag	cac	gca	gcc	ctg	ggc	ttc	ttt	gac	tgc	ctc	cga	gcc	gaa	624
Ala	Ser	Lys	His	Ala	Ala	Leu	Gly	Phe	Phe	Asp	Cys	Leu	Arg	Ala	Glu	
		195					200					205				
gtg	gag	gaa	tac	gat	gtt	gtc	atc	agc	acc	gtg	agc	ccg	act	ttc	atc	672
Val	Glu	Glu	Tyr	Asp	Val	Val	Ile	Ser	Thr	Val	Ser	Pro	Thr	Phe	Ile	
	210					215					220					
cgg	tcg	tac	cac	gtg	tat	cca	gag	caa	gga	aac	tgg	gaa	gct	tcc	att	720
Arg	Ser	Tyr	His	Val	Tyr	Pro	Glu	Gln	Gly	Asn	Trp	Glu	Ala	Ser	Ile	
225					230					235					240	
tgg	aaa	ttc	ttt	ttc	agg	aag	ctg	acc	tac	ggc	gtg	cac	cca	gta	gag	768
Trp	Lys	Phe	Phe	Phe	Arg	Lys	Leu	Thr	Tyr	Gly	Val	His	Pro	Val	Glu	
				245					250					255		
gtg	gcg	gag	gag	gtg	atg	cgc	acc	gtg	cgg	agg	aag	aag	caa	gag	gtg	816
Val	Ala	Glu	Glu	Val	Met	Arg	Thr	Val	Arg	Arg	Lys	Lys	Gln	Glu	Val	
			260				265						270			
ttt	atg	gcc	aac	ccc	atc	ccc	aag	gcc	gcc	gtg	tac	gtc	cgc	acc	ttc	864
Phe	Met	Ala	Asn	Pro	Ile	Pro	Lys	Ala	Ala	Val	Tyr	Val	Arg	Thr	Phe	
		275					280					285				
ttc	ccg	gag	ttc	ttt	ttc	gcc	gtg	gtg	gcc	tgt	ggg	gtg	aag	gag	aag	912
Phe	Pro	Glu	Phe	Phe	Phe	Ala	Val	Val	Ala	Cys	Gly	Val	Lys	Glu	Lys	
	290					295					300					
ctc	aat	gtc	ccg	gag	gag	ggg										933
Leu	Asn	Val	Pro	Glu	Glu	Gly										
305					310											

<210> 7
 <211> 1725
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (281)...(1387)

<221> misc_feature

<222> 1606, 1620, 1631, 1655, 1658, 1666, 1673, 1688, 1705, 1711

<223> n = A,T,C or G

<400> 7

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gggcccctcc aggccagtct gggcacctcg ggatagcggc tgcagccatc agcaggggca 120
gacggcaggt ggcctggttg ctgcagctcc caggatcagc tctgccctcc ccgcaaacgc 180
cagcctcgtc accgctccag ggcacctcca gcagtaacag gtggttgag caggtggcag 240
ccagcccctg gatgagccaa ggtctcttcc ccagccaggc atg gcc gac tct gca 295
                               Met Ala Asp Ser Ala
                               1             5
```

```
cag gcc cag aag ctg gtg tac ctg gtc aca ggg ggc tgt ggc ttc ctg 343
Gln Ala Gln Lys Leu Val Tyr Leu Val Thr Gly Gly Cys Gly Phe Leu
                10                15                20
```

```
gga gag cac gtg gtg cga atg ctg ctg cag cgg gag ccc cgg ctc ggg 391
Gly Glu His Val Val Arg Met Leu Leu Gln Arg Glu Pro Arg Leu Gly
                25                30                35
```

```
gag ctg cgg gtc ttt gac caa cac ctg ggt ccc tgg ctg gag gag ctg 439
Glu Leu Arg Val Phe Asp Gln His Leu Gly Pro Trp Leu Glu Glu Leu
                40                45                50
```

```
aag aca ggg cct gtg agg gtg act gcc atc cag ggg gac gtg acc cag 487
Lys Thr Gly Pro Val Arg Val Thr Ala Ile Gln Gly Asp Val Thr Gln
                55                60                65
```

```
gcc cat gag gtg gca gca gct gtg gcc gga gcc cat gtg gtc atc cac 535
Ala His Glu Val Ala Ala Val Ala Gly Ala His Val Val Ile His
                70                75                80                85
```

```
acg gct ggg ctg gta gac gtg ttt ggc agg gcc agt ccc aag acc atc 583
Thr Ala Gly Leu Val Asp Val Phe Gly Arg Ala Ser Pro Lys Thr Ile
                90                95                100
```

```
cat gag gtc aac gtg cag ggt acc cgg aac gtg atc gag gct tgt gtg 631
His Glu Val Asn Val Gln Gly Thr Arg Asn Val Ile Glu Ala Cys Val
                105                110                115
```

```
cag acc gga aca cgg ttc ctg gtc tac acc agc agc atg gaa gtt gtg 679
Gln Thr Gly Thr Arg Phe Leu Val Tyr Thr Ser Ser Met Glu Val Val
                120                125                130
```

```
ggg cct aac acc aaa ggt cac ccc ttc tac agg ggc aac gaa gac acc 727
Gly Pro Asn Thr Lys Gly His Pro Phe Tyr Arg Gly Asn Glu Asp Thr
                135                140                145
```

```
cca tac gaa gca gtg cac agg cac ccc tat cct tgc agc aag gcc ctg 775
Pro Tyr Glu Ala Val His Arg His Pro Tyr Pro Cys Ser Lys Ala Leu
                150                155                160                165
```

```
gcc gag tgg ctg gtc ctg gag gcc aac ggg agg aag gtc cgt ggg ggg 823
Ala Glu Trp Leu Val Leu Glu Ala Asn Gly Arg Lys Val Arg Gly Gly
                170                175                180
```

```
ctg ccc ctg gtg acg tgt gcc ctt cgt ccc acg ggc atc tac ggt gaa 871
Leu Pro Leu Val Thr Cys Ala Leu Arg Pro Thr Gly Ile Tyr Gly Glu
                185                190                195
```

```
ggc cac cag atc atg agg gac ttc tac cgc cag ggc ctg cgc ctg gga 919
Gly His Gln Ile Met Arg Asp Phe Tyr Arg Gln Gly Leu Arg Leu Gly
                200                205                210
```

ggt tgg ctc ttc cgg gcc atc ccg gcc tct gtg gag cat ggc cgg gtc 967
 Gly Trp Leu Phe Arg Ala Ile Pro Ala Ser Val Glu His Gly Arg Val
 215 220 225
 tat gtg ggc aat gtt gcc tgg atg cac gtg ctg gca gcc cgg gag ctg 1015
 Tyr Val Gly Asn Val Ala Trp Met His Val Leu Ala Ala Arg Glu Leu
 230 235 240 245
 gag cag cgg gca gcc ctg atg ggc gcc cag gta tac ttc tgc tac gat 1063
 Glu Gln Arg Ala Ala Leu Met Gly Gly Gln Val Tyr Phe Cys Tyr Asp
 250 255 260
 gga tca ccc tac agg agc tac gag gat ttc aac atg gag ttc ctg ggc 1111
 Gly Ser Pro Tyr Arg Ser Tyr Glu Asp Phe Asn Met Glu Phe Leu Gly
 265 270 275
 ccc tgc gga ctg cgg ctg gtg ggc gcc cgc cca ttg ctg ccc tac tgg 1159
 Pro Cys Gly Leu Arg Leu Val Gly Ala Arg Pro Leu Leu Pro Tyr Trp
 280 285 290
 ctg ctg gtg ttc ctg gct gcc ctc aat gcc ctg ctg cag tgg ctg ctg 1207
 Leu Leu Val Phe Leu Ala Ala Leu Asn Ala Leu Leu Gln Trp Leu Leu
 295 300 305
 cgg cca ctg gtg ctc tac gca ccc ctg ctg aac ccc tac acg ctg gcc 1255
 Arg Pro Leu Val Leu Tyr Ala Pro Leu Leu Asn Pro Tyr Thr Leu Ala
 310 315 320 325
 gtg gcc aac acc acc ttc acc gtc agc acc gac aag gct cag cgc cat 1303
 Val Ala Asn Thr Thr Phe Thr Val Ser Thr Asp Lys Ala Gln Arg His
 330 335 340
 ttc gcc tat gag ccc ctg ttc tgc tgg gag gat agc cgg acc cgc acc 1351
 Phe Gly Tyr Glu Pro Leu Phe Ser Trp Glu Asp Ser Arg Thr Arg Thr
 345 350 355
 att ctc tgg gta cag gcc gct acg ggt tca gcc cag tgacggtggg 1397
 Ile Leu Trp Val Gln Ala Ala Thr Gly Ser Ala Gln
 360 365
 gctggggcct ggaggccag atacagcaca tccacccagg tcccagagccc tcacaccctg 1457
 gacgggaagg gacagctgca ttccagagca ggaggcaggg ctctggggcc agaattggctg 1517
 tccttgctgt agagccctcc acattttctt tttctttttt gagacagggt cttgctctgt 1577
 caccagact ggaatgcaag tgggtgtgant cataagctca ctngmaccct yaanccttct 1637
 gggttcaagc aatccttntc ngcctyaanc cttctngaac aagcttgga nccacaggtg 1697
 cagccancc acancctggc tttttttt 1725

<210> 8

<211> 369

<212> PRT

<213> Homo sapiens

<400> 8

Met Ala Asp Ser Ala Gln Ala Gln Lys Leu Val Tyr Leu Val Thr Gly
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 Gly Cys Gly Phe Leu Gly Glu His Val Val Arg Met Leu Leu Gln Arg
 20 25 30
 Glu Pro Arg Leu Gly Glu Leu Arg Val Phe Asp Gln His Leu Gly Pro
 35 40 45
 Trp Leu Glu Glu Leu Lys Thr Gly Pro Val Arg Val Thr Ala Ile Gln
 50 55 60
 Gly Asp Val Thr Gln Ala His Glu Val Ala Ala Val Ala Gly Ala
 65 70 75 80

His	Val	Val	Ile	His	Thr	Ala	Gly	Leu	Val	Asp	Val	Phe	Gly	Arg	Ala	
			85						90					95		
Ser	Pro	Lys	Thr	Ile	His	Glu	Val	Asn	Val	Gln	Gly	Thr	Arg	Asn	Val	
			100					105					110			
Ile	Glu	Ala	Cys	Val	Gln	Thr	Gly	Thr	Arg	Phe	Leu	Val	Tyr	Thr	Ser	
			115				120					125				
Ser	Met	Glu	Val	Val	Gly	Pro	Asn	Thr	Lys	Gly	His	Pro	Phe	Tyr	Arg	
			130			135					140					
Gly	Asn	Glu	Asp	Thr	Pro	Tyr	Glu	Ala	Val	His	Arg	His	Pro	Tyr	Pro	
145					150					155					160	
Cys	Ser	Lys	Ala	Leu	Ala	Glu	Trp	Leu	Val	Leu	Glu	Ala	Asn	Gly	Arg	
				165					170					175		
Lys	Val	Arg	Gly	Gly	Leu	Pro	Leu	Val	Thr	Cys	Ala	Leu	Arg	Pro	Thr	
			180					185					190			
Gly	Ile	Tyr	Gly	Glu	Gly	His	Gln	Ile	Met	Arg	Asp	Phe	Tyr	Arg	Gln	
			195				200					205				
Gly	Leu	Arg	Leu	Gly	Gly	Trp	Leu	Phe	Arg	Ala	Ile	Pro	Ala	Ser	Val	
			210			215					220					
Glu	His	Gly	Arg	Val	Tyr	Val	Gly	Asn	Val	Ala	Trp	Met	His	Val	Leu	
225					230					235					240	
Ala	Ala	Arg	Glu	Leu	Glu	Gln	Arg	Ala	Ala	Leu	Met	Gly	Gly	Gln	Val	
				245					250					255		
Tyr	Phe	Cys	Tyr	Asp	Gly	Ser	Pro	Tyr	Arg	Ser	Tyr	Glu	Asp	Phe	Asn	
			260					265					270			
Met	Glu	Phe	Leu	Gly	Pro	Cys	Gly	Leu	Arg	Leu	Val	Gly	Ala	Arg	Pro	
			275			280						285				
Leu	Leu	Pro	Tyr	Trp	Leu	Leu	Val	Phe	Leu	Ala	Ala	Leu	Asn	Ala	Leu	
			290			295					300					
Leu	Gln	Trp	Leu	Leu	Arg	Pro	Leu	Val	Leu	Tyr	Ala	Pro	Leu	Leu	Asn	
305					310					315					320	
Pro	Tyr	Thr	Leu	Ala	Val	Ala	Asn	Thr	Thr	Phe	Thr	Val	Ser	Thr	Asp	
				325					330					335		
Lys	Ala	Gln	Arg	His	Phe	Gly	Tyr	Glu	Pro	Leu	Phe	Ser	Trp	Glu	Asp	
			340				345						350			
Ser	Arg	Thr	Arg	Thr	Ile	Leu	Trp	Val	Gln	Ala	Ala	Thr	Gly	Ser	Ala	
			355				360						365			
Gln																

<210> 9
 <211> 1107
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1107)

<400> 9																
atg	gcc	gac	tct	gca	cag	gcc	cag	aag	ctg	gtg	tac	ctg	gtc	aca	ggg	48
Met	Ala	Asp	Ser	Ala	Gln	Ala	Gln	Lys	Leu	Val	Tyr	Leu	Val	Thr	Gly	
1				5					10					15		
ggc tgt ggc ttc ctg gga gag cac gtg gtg cga atg ctg ctg cag cgg															96	
Gly	Cys	Gly	Phe	Leu	Gly	Glu	His	Val	Val	Arg	Met	Leu	Leu	Gln	Arg	
			20				25						30			
gag ccc cgg ctc ggg gag ctg cgg gtc ttt gac caa cac ctg ggt ccc															144	
Glu	Pro	Arg	Leu	Gly	Glu	Leu	Arg	Val	Phe	Asp	Gln	His	Leu	Gly	Pro	
			35				40					45				
tgg ctg gag gag ctg aag aca ggg cct gtg agg gtg act gcc atc cag															192	
Trp	Leu	Glu	Glu	Leu	Lys	Thr	Gly	Pro	Val	Arg	Val	Thr	Ala	Ile	Gln	

50	55	60	
ggg gac gtg acc cag gcc cat gag gtg gca gca gct gtg gcc gga gcc Gly Asp Val Thr Gln Ala His Glu Val Ala Ala Val Ala Gly Ala 65 70 75 80			240
cat gtg gtc atc cac acg gct ggg ctg gta gac gtg ttt ggc agg gcc His Val Val Ile His Thr Ala Gly Leu Val Asp Val Phe Gly Arg Ala 85 90 95			288
agt ccc aag acc atc cat gag gtc aac gtg cag ggt acc cgg aac gtg Ser Pro Lys Thr Ile His Glu Val Asn Val Gln Gly Thr Arg Asn Val 100 105 110			336
atc gag gct tgt gtg cag acc gga aca cgg ttc ctg gtc tac acc agc Ile Glu Ala Cys Val Gln Thr Gly Thr Arg Phe Leu Val Tyr Thr Ser 115 120 125			384
agc atg gaa gtt gtg ggg cct aac acc aaa ggt cac ccc ttc tac agg Ser Met Glu Val Val Gly Pro Asn Thr Lys Gly His Pro Phe Tyr Arg 130 135 140			432
ggc aac gaa gac acc cca tac gaa gca gtg cac agg cac ccc tat cct Gly Asn Glu Asp Thr Pro Tyr Glu Ala Val His Arg His Pro Tyr Pro 145 150 155 160			480
tgc agc aag gcc ctg gcc gag tgg ctg gtc ctg gag gcc aac ggg agg Cys Ser Lys Ala Leu Ala Glu Trp Leu Val Leu Glu Ala Asn Gly Arg 165 170 175			528
aag gtc cgt ggg ggg ctg ccc ctg gtg acg tgt gcc ctt cgt ccc acg Lys Val Arg Gly Gly Leu Pro Leu Val Thr Cys Ala Leu Arg Pro Thr 180 185 190			576
ggc atc tac ggt gaa ggc cac cag atc atg agg gac ttc tac cgc cag Gly Ile Tyr Gly Glu Gly His Gln Ile Met Arg Asp Phe Tyr Arg Gln 195 200 205			624
ggc ctg cgc ctg gga ggt tgg ctc ttc cgg gcc atc ccg gcc tct gtg Gly Leu Arg Leu Gly Gly Trp Leu Phe Arg Ala Ile Pro Ala Ser Val 210 215 220			672
gag cat ggc cgg gtc tat gtg ggc aat gtt gcc tgg atg cac gtg ctg Glu His Gly Arg Val Tyr Val Gly Asn Val Ala Trp Met His Val Leu 225 230 235 240			720
gca gcc cgg gag ctg gag cag cgg gca gcc ctg atg ggc ggc cag gta Ala Ala Arg Glu Leu Glu Gln Arg Ala Ala Leu Met Gly Gly Gln Val 245 250 255			768
tac ttc tgc tac gat gga tca ccc tac agg agc tac gag gat ttc aac Tyr Phe Cys Tyr Asp Gly Ser Pro Tyr Arg Ser Tyr Glu Asp Phe Asn 260 265 270			816
atg gag ttc ctg ggc ccc tgc gga ctg cgg ctg gtg ggc gcc cgc cca Met Glu Phe Leu Gly Pro Cys Gly Leu Arg Leu Val Gly Ala Arg Pro 275 280 285			864
ttg ctg ccc tac tgg ctg ctg gtg ttc ctg gct gcc ctc aat gcc ctg Leu Leu Pro Tyr Trp Leu Leu Val Phe Leu Ala Leu Asn Ala Leu 290 295 300			912
ctg cag tgg ctg ctg cgg cca ctg gtg ctc tac gca ccc ctg ctg aac Leu Gln Trp Leu Leu Arg Pro Leu Val Leu Tyr Ala Pro Leu Leu Asn 300			960

305	310	315	320	
ccc tac acg ctg gcc gtg gcc aac acc acc ttc acc gtc agc acc gac				1008
Pro Tyr Thr Leu Ala Val Ala Asn Thr Thr Phe Thr Val Ser Thr Asp				
	325	330	335	
aag gct cag cgc cat ttc ggc tat gag ccc ctg ttc tcg tgg gag gat				1056
Lys Ala Gln Arg His Phe Gly Tyr Glu Pro Leu Phe Ser Trp Glu Asp				
	340	345	350	
agc cgg acc cgc acc att ctc tgg gta cag gcc gct acg ggt tca gcc				1104
Ser Arg Thr Arg Thr Ile Leu Trp Val Gln Ala Ala Thr Gly Ser Ala				
	355	360	365	
cag				1107
Gln				

<210> 10
 <211> 1209
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (61)...(1026)

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atg tcc ctg aga ccc aga agg gcc tgc gct cag ctg ctc tgg cac ccc	108
Met Ser Leu Arg Pro Arg Arg Ala Cys Ala Gln Leu Leu Trp His Pro	
1 5 10 15	
gct gca ggg atg gcc tcc tgg gct aag ggc agg agc tac ctg gcg cct	156
Ala Ala Gly Met Ala Ser Trp Ala Lys Gly Arg Ser Tyr Leu Ala Pro	
20 25 30	
ggt ttg ctg cag ggc caa gtg gcc atc gtc acc ggc ggg gcc acg ggc	204
Gly Leu Leu Gln Gly Gln Val Ala Ile Val Thr Gly Gly Ala Thr Gly	
35 40 45	
atc gga aaa gcc atc gtg aag gag ctc ctg gag ctg ggg agt aat gtg	252
Ile Gly Lys Ala Ile Val Lys Glu Leu Leu Glu Leu Gly Ser Asn Val	
50 55 60	
gtc att gca tcc cgt aag ttg gag aga ttg aag tct gcg gca gat gaa	300
Val Ile Ala Ser Arg Lys Leu Glu Arg Leu Lys Ser Ala Ala Asp Glu	
65 70 75 80	
ctg cag gcc aac cta cct ccc aca aag cag gca cga gtc att ccc ata	348
Leu Gln Ala Asn Leu Pro Pro Thr Lys Gln Ala Arg Val Ile Pro Ile	
85 90 95	
caa tgc aac atc cgg aat gag gag gag gtg aat aat ttg gtc aaa tct	396
Gln Cys Asn Ile Arg Asn Glu Glu Glu Val Asn Asn Leu Val Lys Ser	
100 105 110	
acc tta gat act ttt ggt aag atc aat ttc ttg gtg aac aat gga gga	444
Thr Leu Asp Thr Phe Gly Lys Ile Asn Phe Leu Val Asn Asn Gly Gly	
115 120 125	
ggc cag ttt ctt tcc cct gct gaa cac atc agt tct aag gga tgg cac	492
Gly Gln Phe Leu Ser Pro Ala Glu His Ile Ser Ser Lys Gly Trp His	

130	135	140	
gct gtg ctt gag acc aac ctg acg ggt acc ttc tac atg tgc aaa gca			540
Ala Val Leu Glu Thr Asn Leu Thr Gly Thr Phe Tyr Met Cys Lys Ala			
145	150	155	160
ggt tac agc tcc tgg atg aaa gag cat gga gga tct atc gtc aat atc			588
Val Tyr Ser Ser Trp Met Lys Glu His Gly Gly Ser Ile Val Asn Ile			
	165	170	175
att gtc cct act aaa gct gga ttt cca tta gct gtg cat tct gga gct			636
Ile Val Pro Thr Lys Ala Gly Phe Pro Leu Ala Val His Ser Gly Ala			
	180	185	190
gca aga gca ggt gtt tac aac ctc acc aaa tct tta gct ttg gaa tgg			684
Ala Arg Ala Gly Val Tyr Asn Leu Thr Lys Ser Leu Ala Leu Glu Trp			
	195	200	205
gcc tgc agt gga ata cgg atc aat tgt gtt gcc cct gga gtt att tat			732
Ala Cys Ser Gly Ile Arg Ile Asn Cys Val Ala Pro Gly Val Ile Tyr			
	210	215	220
tcc cag act gct gtg gag aac tat ggt tcc tgg gga caa agc ttc ttt			780
Ser Gln Thr Ala Val Glu Asn Tyr Gly Ser Trp Gly Gln Ser Phe Phe			
	225	230	235
gaa ggg tct ttt cag aaa atc ccc gct aaa cga att ggt gtt cct gag			828
Glu Gly Ser Phe Gln Lys Ile Pro Ala Lys Arg Ile Gly Val Pro Glu			
	245	250	255
gag gtc tcc tct gtg gtc tgc ttc cta ctg tct cct gca gct tcc ttc			876
Glu Val Ser Ser Val Val Cys Phe Leu Leu Ser Pro Ala Ala Ser Phe			
	260	265	270
atc act gga cag tcg gtg gat gtg gat ggg ggc cgg agt ctc tat act			924
Ile Thr Gly Gln Ser Val Asp Val Asp Gly Gly Arg Ser Leu Tyr Thr			
	275	280	285
cac tcg tat gag gta cca gat cat gac aac tgg ccc aag gga gca ggg			972
His Ser Tyr Glu Val Pro Asp His Asp Asn Trp Pro Lys Gly Ala Gly			
	290	295	300
gac ctt tct gtt gtc aaa aag atg aag gag acc tta aag gag aaa gct			1020
Asp Leu Ser Val Val Lys Lys Met Lys Glu Thr Leu Lys Glu Lys Ala			
	305	310	315
aag ctc tgagctgagg aaacaaggtg tcttccatcc ccagtgcctt cacatcttga			1076
Lys Leu			

ggatatgctt ctgtactttt taaaagctta tagttggtat ggaaaacatt tttcttattt	1136
ttaagtgtta ttaattatat ctatggaaaa actattcctg aaatatatac agtcttatgt	1196
ccccaaaaaa aaa	1209

<210> 11
 <211> 322
 <212> PRT
 <213> Homo sapiens

<400> 11	
Met Ser Leu Arg Pro Arg Arg Ala Cys Ala Gln Leu Leu Trp His Pro	
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Ala Ala Gly Met Ala Ser Trp Ala Lys Gly Arg Ser Tyr Leu Ala Pro	
20 25 30	

Gly	Leu	Leu	Gln	Gly	Gln	Val	Ala	Ile	Val	Thr	Gly	Gly	Ala	Thr	Gly
	35						40					45			
Ile	Gly	Lys	Ala	Ile	Val	Lys	Glu	Leu	Leu	Glu	Leu	Gly	Ser	Asn	Val
	50					55					60				
Val	Ile	Ala	Ser	Arg	Lys	Leu	Glu	Arg	Leu	Lys	Ser	Ala	Ala	Asp	Glu
	65				70					75				80	
Leu	Gln	Ala	Asn	Leu	Pro	Pro	Thr	Lys	Gln	Ala	Arg	Val	Ile	Pro	Ile
			85						90					95	
Gln	Cys	Asn	Ile	Arg	Asn	Glu	Glu	Glu	Val	Asn	Asn	Leu	Val	Lys	Ser
		100						105					110		
Thr	Leu	Asp	Thr	Phe	Gly	Lys	Ile	Asn	Phe	Leu	Val	Asn	Asn	Gly	Gly
	115					120						125			
Gly	Gln	Phe	Leu	Ser	Pro	Ala	Glu	His	Ile	Ser	Ser	Lys	Gly	Trp	His
	130					135					140				
Ala	Val	Leu	Glu	Thr	Asn	Leu	Thr	Gly	Thr	Phe	Tyr	Met	Cys	Lys	Ala
	145				150					155					160
Val	Tyr	Ser	Ser	Trp	Met	Lys	Glu	His	Gly	Gly	Ser	Ile	Val	Asn	Ile
			165						170					175	
Ile	Val	Pro	Thr	Lys	Ala	Gly	Phe	Pro	Leu	Ala	Val	His	Ser	Gly	Ala
		180						185						190	
Ala	Arg	Ala	Gly	Val	Tyr	Asn	Leu	Thr	Lys	Ser	Leu	Ala	Leu	Glu	Trp
	195					200						205			
Ala	Cys	Ser	Gly	Ile	Arg	Ile	Asn	Cys	Val	Ala	Pro	Gly	Val	Ile	Tyr
	210					215					220				
Ser	Gln	Thr	Ala	Val	Glu	Asn	Tyr	Gly	Ser	Trp	Gly	Gln	Ser	Phe	Phe
	225				230					235					240
Glu	Gly	Ser	Phe	Gln	Lys	Ile	Pro	Ala	Lys	Arg	Ile	Gly	Val	Pro	Glu
			245						250					255	
Glu	Val	Ser	Ser	Val	Val	Cys	Phe	Leu	Leu	Ser	Pro	Ala	Ala	Ser	Phe
		260						265					270		
Ile	Thr	Gly	Gln	Ser	Val	Asp	Val	Asp	Gly	Gly	Arg	Ser	Leu	Tyr	Thr
	275					280						285			
His	Ser	Tyr	Glu	Val	Pro	Asp	His	Asp	Asn	Trp	Pro	Lys	Gly	Ala	Gly
	290					295					300				
Asp	Leu	Ser	Val	Val	Lys	Lys	Met	Lys	Glu	Thr	Leu	Lys	Glu	Lys	Ala
	305				310					315					320
Lys	Leu														

<210> 12
 <211> 966
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(966)

<400> 12																
atg	tcc	ctg	aga	ccc	aga	agg	gcc	tgc	gct	cag	ctg	ctc	tgg	cac	ccc	48
Met	Ser	Leu	Arg	Pro	Arg	Arg	Ala	Cys	Ala	Gln	Leu	Leu	Trp	His	Pro	
1				5					10					15		
gct gca ggg atg gcc tcc tgg gct aag ggc agg agc tac ctg gcg cct															96	
Ala	Ala	Gly	Met	Ala	Ser	Trp	Ala	Lys	Gly	Arg	Ser	Tyr	Leu	Ala	Pro	
			20					25					30			
ggc ttg ctg cag ggc caa gtg gcc atc gtc acc ggc ggg gcc acg ggc															144	
Gly	Leu	Leu	Gln	Gly	Gln	Val	Ala	Ile	Val	Thr	Gly	Gly	Ala	Thr	Gly	
	35						40					45				
atc gga aaa gcc atc gtg aag gag ctc ctg gag ctg ggg agt aat gtg															192	
Ile	Gly	Lys	Ala	Ile	Val	Lys	Glu	Leu	Leu	Glu	Leu	Gly	Ser	Asn	Val	

50	55	60	
gtc att gca tcc cgt aag ttg gag aga ttg aag tct gcg gca gat gaa Val Ile Ala Ser Arg Lys Leu Glu Arg Leu Lys Ser Ala Ala Asp Glu 65 70 75 80			240
ctg cag gcc aac cta cct ccc aca aag cag gca cga gtc att ccc ata Leu Gln Ala Asn Leu Pro Pro Thr Lys Gln Ala Arg Val Ile Pro Ile 85 90 95			288
caa tgc aac atc cgg aat gag gag gag gtg aat aat ttg gtc aaa tct Gln Cys Asn Ile Arg Asn Glu Glu Glu Val Asn Asn Leu Val Lys Ser 100 105 110			336
acc tta gat act ttt ggt aag atc aat ttc ttg gtg aac aat gga gga Thr Leu Asp Thr Phe Gly Lys Ile Asn Phe Leu Val Asn Asn Gly Gly 115 120 125			384
ggc cag ttt ctt tcc cct gct gaa cac atc agt tct aag gga tgg cac Gly Gln Phe Leu Ser Pro Ala Glu His Ile Ser Ser Lys Gly Trp His 130 135 140			432
gct gtg ctt gag acc aac ctg acg ggt acc ttc tac atg tgc aaa gca Ala Val Leu Glu Thr Asn Leu Thr Gly Thr Phe Tyr Met Cys Lys Ala 145 150 155 160			480
gtt tac agc tcc tgg atg aaa gag cat gga gga tct atc gtc aat atc Val Tyr Ser Ser Trp Met Lys Glu His Gly Gly Ser Ile Val Asn Ile 165 170 175			528
att gtc cct act aaa gct gga ttt cca tta gct gtg cat tct gga gct Ile Val Pro Thr Lys Ala Gly Phe Pro Leu Ala Val His Ser Gly Ala 180 185 190			576
gca aga gca ggt gtt tac aac ctg acc aaa tct tta gct ttg gaa tgg Ala Arg Ala Gly Val Tyr Asn Leu Thr Lys Ser Leu Ala Leu Glu Trp 195 200 205			624
gcc tgc agt gga ata cgg atc aat tgt gtt gcc cct gga gtt att tat Ala Cys Ser Gly Ile Arg Ile Asn Cys Val Ala Pro Gly Val Ile Tyr 210 215 220			672
tcc cag act gct gtg gag aac tat ggt tcc tgg gga caa agc ttc ttt Ser Gln Thr Ala Val Glu Asn Tyr Gly Ser Trp Gly Gln Ser Phe Phe 225 230 235 240			720
gaa ggg tct ttt cag aaa atc ccc gct aaa cga att ggt gtt cct gag Glu Gly Ser Phe Gln Lys Ile Pro Ala Lys Arg Ile Gly Val Pro Glu 245 250 255			768
gag gtc tcc tct gtg gtc tgc ttc cta ctg tct cct gca gct tcc ttc Glu Val Ser Ser Val Val Cys Phe Leu Leu Ser Pro Ala Ala Ser Phe 260 265 270			816
atc act gga cag tgc gtg gat gtg gat ggg ggc cgg agt ctc tat act Ile Thr Gly Gln Ser Val Asp Val Asp Gly Gly Arg Ser Leu Tyr Thr 275 280 285			864
cac tgc tat gag gta cca gat cat gac aac tgg ccc aag gga gca ggg His Ser Tyr Glu Val Pro Asp His Asp Asn Trp Pro Lys Gly Ala Gly 290 295 300			912
gac ctt tct gtt gtc aaa aag atg aag gag acc tta aag gag aaa gct Asp Leu Ser Val Val Lys Lys Met Lys Glu Thr Leu Lys Glu Lys Ala 305 310 315 320			960

305

310

315

320

aag ctc
Lys Leu

966

<210> 13
<211> 303
<212> PRT
<213> Rattus norvegicus

<400> 13

Met	Gly	Ser	Trp	Lys	Ser	Gly	Gln	Ser	Tyr	Leu	Ala	Ala	Gly	Leu	Leu
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Gln	Asn	Gln	Val	Ala	Val	Val	Thr	Gly	Gly	Ala	Thr	Gly	Ile	Gly	Lys
			20					25					30		
Ala	Ile	Ser	Arg	Glu	Leu	Leu	His	Leu	Gly	Cys	Asn	Val	Val	Ile	Ala
		35					40					45			
Ser	Arg	Lys	Leu	Asp	Arg	Leu	Thr	Ala	Ala	Val	Asp	Glu	Leu	Arg	Ala
	50					55					60				
Ser	Gln	Pro	Pro	Ser	Ser	Ser	Thr	Gln	Val	Thr	Ala	Ile	Gln	Cys	Asn
65					70					75				80	
Ile	Arg	Lys	Glu	Glu	Val	Asn	Asn	Leu	Val	Lys	Ser	Thr	Leu	Ala	
			85					90					95		
Lys	Tyr	Gly	Lys	Ile	Asn	Phe	Leu	Val	Asn	Asn	Ala	Gly	Gly	Gln	Phe
			100					105					110		
Met	Ala	Pro	Ala	Glu	Asp	Ile	Thr	Ala	Lys	Gly	Trp	Gln	Ala	Val	Ile
	115						120					125			
Glu	Thr	Asn	Leu	Thr	Gly	Thr	Phe	Tyr	Met	Cys	Lys	Ala	Val	Tyr	Asn
	130					135					140				
Ser	Trp	Met	Lys	Asp	His	Gly	Gly	Ser	Ile	Val	Asn	Ile	Ile	Val	Leu
145					150					155					160
Leu	Asn	Asn	Gly	Phe	Pro	Thr	Ala	Ala	His	Ser	Gly	Ala	Ala	Arg	Ala
			165					170						175	
Gly	Val	Tyr	Asn	Leu	Thr	Lys	Thr	Met	Ala	Leu	Thr	Trp	Ala	Ser	Ser
			180					185					190		
Gly	Val	Arg	Ile	Asn	Cys	Val	Ala	Pro	Gly	Thr	Ile	Tyr	Ser	Gln	Thr
	195						200					205			
Ala	Val	Asp	Asn	Tyr	Gly	Glu	Leu	Gly	Gln	Thr	Met	Phe	Glu	Met	Ala
	210					215				220					
Phe	Glu	Asn	Ile	Pro	Ala	Lys	Arg	Val	Gly	Leu	Pro	Glu	Glu	Ile	Ser
225					230					235				240	
Pro	Leu	Val	Cys	Phe	Leu	Leu	Ser	Pro	Ala	Ala	Ser	Phe	Ile	Thr	Gly
			245						250					255	
Gln	Leu	Ile	Asn	Val	Asp	Gly	Gly	Gln	Ala	Leu	Tyr	Thr	Arg	Asn	Phe
			260					265					270		
Thr	Ile	Pro	Asp	His	Asp	Asn	Trp	Pro	Val	Gly	Ala	Gly	Asp	Ser	Ser
	275					280						285			
Phe	Ile	Lys	Lys	Val	Lys	Glu	Ser	Leu	Lys	Lys	Gln	Ala	Arg	Leu	
	290					295					300				

<210> 14
<211> 1108
<212> DNA
<213> Mus musculus

<220>

<221> CDS

<222> (102)...(1034)

<400> 14

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agg aag cta gcc tat ggc gtg cac ccg gtg gag gtg gct gag gaa gtg 884
Arg Lys Leu Ala Tyr Gly Val His Pro Val Glu Val Ala Glu Glu Val
250 255 260

atg cgc aca gta cgg agg aag aag caa gag gtg ttc atg gcc aac ccg 932
Met Arg Thr Val Arg Arg Lys Lys Gln Glu Val Phe Met Ala Asn Pro
265 270 275

gtt cct aag gct gcc gtg ttc atc cgc acc ttc ttc cct gag ttc ttc 980
Val Pro Lys Ala Ala Val Phe Ile Arg Thr Phe Phe Pro Glu Phe Phe
280 285 290

ttc gct gtg gtg gcc tgt ggg gtg aag gag aag ctc aat gtc cca gaa 1028
Phe Ala Val Val Ala Cys Gly Val Lys Glu Lys Leu Asn Val Pro Glu
295 300 305

gag ggt taacctcgtg gccaaagggg tcactcaagg ggaataaagg ctttcctaga 1084
Glu Gly
310

gaaaaaaaaa aaaaaaaaaa aaaa 1108

<210> 15
<211> 311
<212> PRT
<213> Mus musculus

<400> 15
Met Gly Leu Met Ala Val Leu Met Leu Pro Leu Leu Leu Leu Gly Ile
1 5 10 15
Ser Gly Leu Leu Phe Ile Tyr Gln Glu Ala Ser Arg Leu Trp Ser Lys
20 25 30
Ser Ala Val Gln Asn Lys Val Val Val Ile Thr Asp Ala Ile Ser Gly
35 40 45
Leu Gly Lys Glu Cys Ala Arg Val Phe His Ala Gly Gly Ala Arg Leu
50 55 60
Val Leu Cys Gly Lys Asn Trp Glu Gly Leu Glu Ser Leu Tyr Ala Thr
65 70 75 80
Leu Thr Ser Val Ala Asp Pro Ser Lys Thr Phe Thr Pro Lys Leu Val
85 90 95
Leu Leu Asp Leu Ser Asp Ile Ser Cys Val Gln Asp Val Ala Lys Glu
100 105 110
Val Leu Asp Cys Tyr Gly Cys Val Asp Ile Leu Ile Asn Asn Ala Ser
115 120 125
Val Lys Val Lys Gly Pro Ala His Lys Ile Ser Leu Glu Leu Asp Lys
130 135 140
Lys Ile Met Asp Ala Asn Tyr Phe Gly Pro Ile Thr Leu Thr Lys Val
145 150 155 160
Leu Leu Pro Asn Met Ile Ser Arg Arg Thr Gly Gln Ile Val Leu Val
165 170 175
Asn Asn Ile Gln Ala Lys Phe Gly Ile Pro Phe Arg Thr Ala Tyr Ala
180 185 190
Ala Ser Lys His Ala Val Met Gly Phe Phe Asp Cys Leu Arg Ala Glu
195 200 205
Val Glu Glu Tyr Asp Val Val Val Ser Thr Val Ser Pro Thr Phe Ile
210 215 220
Arg Ser Tyr Arg Ala Ser Pro Glu Gln Arg Asn Trp Glu Thr Ser Ile
225 230 235 240
Cys Lys Phe Phe Cys Arg Lys Leu Ala Tyr Gly Val His Pro Val Glu
245 250 255
Val Ala Glu Glu Val Met Arg Thr Val Arg Arg Lys Lys Gln Glu Val
260 265 270
Phe Met Ala Asn Pro Val Pro Lys Ala Ala Val Phe Ile Arg Thr Phe
275 280 285

Phe Pro Glu Phe Phe Phe Ala Val Val Ala Cys Gly Val Lys Glu Lys
 290 295 300
 Leu Asn Val Pro Glu Glu Gly
 305 310

<210> 16
 <211> 933
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(933)

<400> 16
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 Met Gly Leu Met Ala Val Leu Met Leu Pro Leu Leu Leu Leu Gly Ile
 1 5 10 15
 agc ggc ctc ctc ttc att tac cag gag gca tcc agg ctg tgg tgc aag 96
 Ser Gly Leu Leu Phe Ile Tyr Gln Glu Ala Ser Arg Leu Trp Ser Lys
 20 25 30
 tct gcc gtg cag aac aaa gtg gtg gtc atc aca gat gcc atc tca gga 144
 Ser Ala Val Gln Asn Lys Val Val Val Ile Thr Asp Ala Ile Ser Gly
 35 40 45
 ctg gga aag gag tgt gct cgg gtg ttc cat gca ggt ggg gca agg ctg 192
 Leu Gly Lys Glu Cys Ala Arg Val Phe His Ala Gly Gly Ala Arg Leu
 50 55 60
 gtg ctg tgt gga aag aac tgg gag gga ctg gag agc ctc tat gcc acc 240
 Val Leu Cys Gly Lys Asn Trp Glu Gly Leu Glu Ser Leu Tyr Ala Thr
 65 70 75 80
 ttg acc agt gtg gct gac ccc agc aag aca ttc acc ccc aag ctg gtc 288
 Leu Thr Ser Val Ala Asp Pro Ser Lys Thr Phe Thr Pro Lys Leu Val
 85 90 95
 ctc ctg gat ctc tca gac att agc tgt gtt caa gat gtg gcc aaa gag 336
 Leu Leu Asp Leu Ser Asp Ile Ser Cys Val Gln Asp Val Ala Lys Glu
 100 105 110
 gtc ctg gac tgc tac ggc tgt gtg gac atc ctc atc aac aat gcc agc 384
 Val Leu Asp Cys Tyr Gly Cys Val Asp Ile Leu Ile Asn Asn Ala Ser
 115 120 125
 gtg aaa gtg aag ggg cct gcc cac aag att tcc ctg gag ctt gac aaa 432
 Val Lys Val Lys Gly Pro Ala His Lys Ile Ser Leu Glu Leu Asp Lys
 130 135 140
 aag atc atg gat gcc aac tac ttc gga ccc atc act tta acc aaa gtt 480
 Lys Ile Met Asp Ala Asn Tyr Phe Gly Pro Ile Thr Leu Thr Lys Val
 145 150 155 160
 ctg ctt ccc aac atg atc tcc agg aga aca ggc cag att gtg tta gtg 528
 Leu Leu Pro Asn Met Ile Ser Arg Arg Thr Gly Gln Ile Val Leu Val
 165 170 175
 aac aac atc caa gcg aag ttt gga atc ccg ttc cgc aca gct tat gca 576
 Asn Asn Ile Gln Ala Lys Phe Gly Ile Pro Phe Arg Thr Ala Tyr Ala
 180 185 190

gcc tct aag cat gcc gtc atg ggc ttc ttt gac tgc ctc cga gcc gag	624
Ala Ser Lys His Ala Val Met Gly Phe Phe Asp Cys Leu Arg Ala Glu	
195 200 205	
gtt gag gaa tac gat gtt gtg gtc agc acc gtg agc cca act ttc atc	672
Val Glu Glu Tyr Asp Val Val Val Ser Thr Val Ser Pro Thr Phe Ile	
210 215 220	
cgc tcc tac cgt gct tcc cct gag caa aga aac tgg gag aca tcc att	720
Arg Ser Tyr Arg Ala Ser Pro Glu Gln Arg Asn Trp Glu Thr Ser Ile	
225 230 235 240	
tgt aaa ttc ttc tgc agg aag cta gcc tat ggc gtg cac ccg gtg gag	768
Cys Lys Phe Phe Cys Arg Lys Leu Ala Tyr Gly Val His Pro Val Glu	
245 250 255	
gtg gct gag gaa gtg atg cgc aca gta cgg agg aag aag caa gag gtg	816
Val Ala Glu Glu Val Met Arg Thr Val Arg Arg Lys Lys Gln Glu Val	
260 265 270	
ttc atg gcc aac ccg gtt cct aag gct gcc gtg ttc atc cgc acc ttc	864
Phe Met Ala Asn Pro Val Pro Lys Ala Ala Val Phe Ile Arg Thr Phe	
275 280 285	
ttc cct gag ttc ttc ttc gct gtg gtg gcc tgt ggg gtg aag gag aag	912
Phe Pro Glu Phe Phe Phe Ala Val Val Ala Cys Gly Val Lys Glu Lys	
290 295 300	
ctc aat gtc cca gaa gag ggt	933
Leu Asn Val Pro Glu Glu Gly	
305 310	

<210> 17

<211> 491

<212> PRT

<213> Artificial Sequence

<220>

<223> aldehyde dehydrogenase domain

<400> 17

Glu Trp Val Asp Ser Ala Ser Gly Lys Thr Phe Glu Val Val Asn Pro	
1 5 10 15	
Ala Asn Lys Gly Glu Val Ile Gly Arg Val Pro Glu Ala Thr Ala Glu	
20 25 30	
Asp Val Asp Ala Ala Val Lys Ala Ala Lys Glu Ala Phe Lys Ser Gly	
35 40 45	
Pro Trp Trp Ala Lys Val Pro Ala Ser Glu Arg Ala Arg Ile Leu Arg	
50 55 60	
Lys Leu Ala Asp Leu Ile Glu Glu Arg Glu Asp Glu Leu Ala Ala Leu	
65 70 75 80	
Glu Thr Leu Asp Leu Gly Lys Pro Leu Ala Glu Ala Lys Gly Asp Thr	
85 90 95	
Glu Val Gly Arg Ala Ile Asp Glu Ile Arg Tyr Tyr Ala Gly Trp Ala	
100 105 110	
Arg Lys Leu Met Gly Glu Arg Arg Val Ile Pro Ser Leu Ala Thr Asp	
115 120 125	
Gly Asp Glu Glu Leu Asn Tyr Thr Arg Arg Glu Pro Leu Gly Val Val	
130 135 140	
Gly Val Ile Ser Pro Trp Asn Phe Pro Leu Leu Leu Ala Leu Trp Lys	
145 150 155 160	
Leu Ala Pro Ala Leu Ala Ala Gly Asn Thr Val Val Leu Lys Pro Ser	

<223> Xaa = Any Amino Acid

<221> VARIANT

<222> 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450,
488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499,
500, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526,
527, 528, 529

<223> Xaa = Any Amino Acid

<400> 18

Arg	Ala	Gln	His	Leu	Thr	Arg	Leu	Ala	Glu	Val	Ile	Gln	Lys	His	Gln
1				5					10					15	
Arg	Leu	Leu	Trp	Thr	Leu	Glu	Ser	Leu	Val	Thr	Gly	Arg	Ala	Val	Arg
			20					25					30		
Glu	Val	Arg	Asp	Gly	Asp	Val	Gln	Leu	Ala	Gln	Gln	Leu	Leu	His	Tyr
		35					40					45			
His	Ala	Ile	Gln	Ala	Ser	Thr	Gln	Glu	Glu	Ala	Leu	Ala	Gly	Trp	Glu
	50					55					60				
Pro	Met	Gly	Val	Ile	Gly	Leu	Ile	Leu	Pro	Pro	Thr	Phe	Ser	Phe	Leu
65					70					75					80
Glu	Met	Met	Trp	Arg	Ile	Cys	Pro	Ala	Leu	Ala	Val	Gly	Val	Thr	Xaa
				85					90					95	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			100					105					110		
Xaa	Xaa	Gly	Glu	Leu	Gly	Pro	Phe	Pro	Gly	Ile	Leu	Asn	Val	Val	Ser
		115					120					125			
Gly	Pro	Ala	Ser	Leu	Val	Pro	Ile	Leu	Ala	Ser	Gln	Pro	Gly	Ile	Arg
	130					135					140				
Lys	Val	Ala	Phe	Cys	Gly	Ala	Pro	Glu	Glu	Gly	Arg	Ala	Leu	Arg	Arg
145					150					155					160
Ser	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				165					170					175	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Thr	Ala	Asp	Val	Asp	Ser	Ala	Val	Glu
			180					185					190		
Gly	Val	Val	Asp	Ala	Ala	Trp	Ser	Asp	Pro	Gly	Pro	Gly	Gly	Leu	Arg
	195					200					205				
Leu	Leu	Ile	Gln	Glu	Ser	Val	Trp	Asp	Glu	Ala	Met	Arg	Arg	Leu	Gln
	210					215					220				
Glu	Arg	Met	Gly	Arg	Leu	Arg	Ser	Gly	Arg	Gly	Leu	Asp	Gly	Ala	Val
225					230					235					240
Asp	Met	Gly	Ala	Arg	Gly	Ala	Ala	Ala	Cys	Asp	Leu	Val	Gln	Arg	Phe
			245						250					255	
Val	Arg	Glu	Ala	Gln	Ser	Gln	Gly	Ala	Gln	Val	Phe	Gln	Ala	Gly	Asp
			260					265					270		
Val	Pro	Ser	Glu	Arg	Pro	Phe	Tyr	Pro	Pro	Thr	Leu	Val	Ser	Asn	Leu
	275						280					285			
Pro	Pro	Ala	Ser	Pro	Cys	Ala	Gln	Val	Glu	Val	Pro	Trp	Pro	Val	Val
	290					295					300				
Val	Ala	Ser	Pro	Phe	Arg	Thr	Ala	Lys	Glu	Ala	Leu	Leu	Val	Ala	Asn
305					310					315					320
Gly	Thr	Pro	Arg	Gly	Gly	Ser	Ala	Ser	Val	Trp	Ser	Glu	Arg	Leu	Gly
			325						330					335	
Gln	Ala	Leu	Glu	Leu	Gly	Tyr	Gly	Leu	Gln	Val	Gly	Thr	Val	Trp	Ile
		340					345						350		
Asn	Ala	His	Gly	Leu	Arg	Asp	Pro	Ser	Val	Pro	Thr	Gly	Gly	Cys	Lys
	355						360					365			
Glu	Ser	Gly	Cys	Ser	Trp	His	Gly	Gly	Pro	Asp	Gly	Leu	Tyr	Glu	Tyr
	370					375					380				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
385					390					395					400
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				405					410					415	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			420				425						430		

Leu Thr Arg Ser Leu Ala Leu Glu Leu Ala Pro His Gly Ile Arg Val
180 185 190
Asn Ala Val Ala Pro Gly Gly Val Asp Thr Asp
195 200

<210> 20
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> alpha2 macroglobulin family domain

<400> 20
Ile Asp Glu Asp Asp Ile Thr Ile Arg Ser Tyr Phe Pro Glu
1 5 10

<210> 21
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> oxidoreductase protein dehydrogenase

<400> 21
Asp Leu Ser Asp Ile Ser Cys Val Pro Asp Val Ala Lys Glu Val Leu
1 5 10 15
Asp Cys Tyr Gly Cys Val Asp Ile Leu Ile Asn Asn Ala Ser Val Lys
20 25 30
Val Lys Gly Pro Ala His Lys Ile Ser Leu Glu Leu Asp Lys Lys Ile
35 40 45
Met Asp Ala Asn Tyr Phe Gly Pro Ile Leu Thr Leu Thr Lys Ala Leu
50 55 60
Leu Pro Asn Met Ile Ser Arg Arg Thr Gly Gln Ile Val Leu Val Asn
65 70 75 80
Asn Ile Gln Gly Lys Phe Gly Ile Pro Phe Arg Thr Thr Tyr Ala Ala
85 90 95
Ser Lys His Ala Ala Ser Lys His Ala Ala Leu Gly Phe Phe Asp Cys
100 105 110
Leu Arg Ala Glu Val Glu Glu Tyr Asp Val Val Ile Ser Thr Val
115 120 125

<210> 22
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> S-adenosylmethionine synthetase domain

<400> 22
His Phe Gly Arg Glu Glu Val Asp Phe Pro Trp Glu
1 5 10

<210> 23
 <211> 424
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 3-beta hydroxysteroid dehydrogenase domain

<400> 23
 Glu Leu Ser Glu Ser Leu Asp Met Ala Gly Leu Ser Cys Leu Val Thr
 1 5 10 15
 Gly Gly Gly Gly Phe Leu Gly Arg His Ile Val Arg Glu Leu Leu Arg
 20 25 30
 Glu Gly Glu Ser Leu Gln Glu Val Arg Val Phe Asp Leu Arg Phe Ser
 35 40 45
 Pro Glu Leu Asp Glu Asp Ser Ser Lys Leu Gln Val Ile Thr Lys Ile
 50 55 60
 Lys Tyr Ile Glu Gly Asp Val Thr Asp Lys Gln Asp Leu Ala Ala Ala
 65 70 75 80
 Leu Gln Gly Ile Ser Cys Cys Thr Leu Leu Asp Met Thr Leu Met Asp
 85 90 95
 Asp Val Val Ile His Thr Ala Ala Ile Ile Asp Val Phe Gly Glu Leu
 100 105 110
 Arg Val Ser Gly Ser Asp Leu Ser Phe Gly Val Thr Val Leu Phe Leu
 115 120 125
 Ala Val Thr Glu Gly Ser Tyr Val Val Phe Tyr Met Gly Ala Thr Asp
 130 135 140
 Leu Arg Lys Ala Ser Arg Asp Arg Ile Met Lys Val Asn Val Lys Gly
 145 150 155 160
 Thr Gln Asn Val Leu Asp Ala Cys Val Glu Ala Gly Val Arg Val Leu
 165 170 175
 Val Tyr Thr Ser Ser Met Glu Val Val Gly Pro Asn Ser Arg Gly Gln
 180 185 190
 Pro Ile Val Asn Gly Asp Glu Thr Thr Pro Tyr Glu Ser Thr Asp Asp
 195 200 205
 His Gln Asp Ala Tyr Pro Glu Ser Lys Ala Leu Ala Glu Lys Leu Val
 210 215 220
 Leu Lys Ala Asn Gly Ser Met Leu Lys Asn Gly Gly Arg Leu Tyr Thr
 225 230 235 240
 Cys Ala Leu Arg Pro Ala Gly Ile Phe Glu Gly Asp Gln Phe Leu Val
 245 250 255
 Pro Phe Leu Arg Gln Leu Val Lys Asn Gly Leu Ala Lys Phe Arg Ile
 260 265 270
 Gly Asp Lys Asn Ala Leu Ser Asp Arg Val Tyr Val Gly Asn Val Ala
 275 280 285
 Trp Ala His Ile Leu Ala Ala Arg Ala Leu Gln Asp Pro Lys Lys Gly
 290 295 300
 Arg Glu Gly Ala Ser Ser Ile Ala Gly Gln Ala Tyr Phe Ile Ser Asp
 305 310 315 320
 Asp Ser Pro Val Asn Ser Tyr Asp Asp Phe Asn Arg Thr Leu Leu Lys
 325 330 335
 Ala Leu Gly Leu Arg Leu Pro Ser Thr Trp Arg Leu Pro Leu Pro Leu
 340 345 350
 Leu Tyr Val Leu Ala Tyr Leu Asn Glu Leu Leu Ser Trp Leu Leu Arg
 355 360 365
 Lys Leu Ala Leu Arg Tyr Thr Pro Leu Leu Asn Pro Tyr Thr Val Thr
 370 375 380
 Leu Ala Asn Thr Thr Phe Thr Phe Ser Thr Asn Lys Ala Lys Lys Asp
 385 390 395 400
 Leu Gly Tyr Glu Pro Leu Val Thr Trp Glu Glu Ala Arg Ala Lys Thr
 405 410 415
 Ile Glu Trp Ile Gln Glu Leu Glu

<210> 24
 <211> 359
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> NAD dependent epimerase/dehydratase domain

<400> 24
 Ile Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Arg
 1 5 10 15
 Glu Leu Leu Asn Asn Tyr Gly Asp Asp Lys Val Val Val Leu Asp Asn
 20 25 30
 Leu Thr Asp Tyr Tyr Gln Tyr Ala Gly Asn Glu Ala Arg Leu Glu Val
 35 40 45
 Val Glu Gly Asn Pro Arg Tyr Thr Phe Val Lys Gly Asp Ile Cys Asp
 50 55 60
 Arg Asp Leu Leu Asp Lys Val Phe Ala Glu His Gln Pro Asp Ala Val
 65 70 75 80
 Ile His Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Glu Lys Pro
 85 90 95
 Leu Ala Tyr Ile Asp Thr Asn Val Val Gly Thr Leu Thr Leu Leu Glu
 100 105 110
 Ala Ala Arg Asn Tyr Trp Ser Ala Leu Asp Glu Thr Lys Ala Gly Val
 115 120 125
 Lys Lys Phe Val Phe Ser Ser Thr Asp Glu Val Tyr Gly Asp Leu Glu
 130 135 140
 Ser Ile Pro Ile Ser Ala Phe Thr Glu Asp Thr Pro Tyr Asn Pro Ser
 145 150 155 160
 Ser Pro Tyr Gly Ala Ser Lys Ala Ser Ser Glu Leu Leu Val Arg Ala
 165 170 175
 Tyr His Arg Ala Tyr Gly Leu Pro Ala Ile Ile Leu Arg Tyr Phe Asn
 180 185 190
 Val Tyr Gly Pro Tyr Gln Ser Gly Arg Ile Gly Glu Asp Pro Asn Gly
 195 200 205
 Phe Pro Glu Lys Leu Ile Pro Leu Ile Ile Gln Asn Ala Leu Gly Lys
 210 215 220
 Gly Glu Pro Leu Pro Val Tyr Gly Asp Gly Tyr Pro Thr Pro Asp Gly
 225 230 235 240
 Thr Gln Val Arg Asp Trp Ile His Val Glu Asp His Ala Arg Ala Asn
 245 250 255
 His Leu Leu Ala Leu Thr Lys Gly Arg Ala Gly Lys Gly Ser Glu Val
 260 265 270
 Tyr Asn Ile Gly Gly Gly Asn Glu Tyr Ser Asn Leu Glu Val Val Glu
 275 280 285
 Ala Ile Glu Lys Leu Leu Gly Glu Leu Ala Pro Glu Lys Pro His Val
 290 295 300
 Lys Ala Lys Glu Asp Pro Ala Thr Phe Val Asp Asp Arg Pro Gly Asp
 305 310 315 320
 Asp Ala Arg Tyr Ala Ala Asp Ala Ser Lys Ile Lys Arg Glu Leu Gly
 325 330 335
 Trp Lys Pro Glu Val Thr Asn Leu Glu Glu Gly Leu Ala Asp Thr Val
 340 345 350
 Asn Trp Tyr Leu Glu Asn Glu
 355

<210> 25
 <211> 260

<212> PRT
<213> Artificial Sequence

<220>
<223> 3-beta hydroxysteroid dehydrogenase delta5 domain

<221> VARIANT
<222> 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150,
192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203,
204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215,
216, 217
<223> Xaa = Any Amino Acid

<400> 25
His Glu Val Asn Val Gln Gly Thr Arg Asn Val Ile Glu Ala Cys Val
1 5 10 15
Gln Thr Gly Thr Arg Phe Leu Val Tyr Thr Ser Ser Met Glu Val Val
20 25 30
Gly Pro Asn Thr Lys Gly His Pro Phe Tyr Arg Gly Asn Glu Asp Thr
35 40 45
Pro Tyr Glu Ala Val His Arg His Pro Tyr Pro Cys Ser Lys Ala Leu
50 55 60
Ala Glu Trp Leu Val Leu Glu Ala Asn Gly Arg Lys Val Arg Gly Gly
65 70 75 80
Leu Pro Leu Val Thr Cys Ala Leu Arg Pro Thr Gly Ile Tyr Gly Glu
85 90 95
Gly His Gln Ile Met Arg Asp Phe Tyr Arg Gln Gly Leu Arg Leu Gly
100 105 110
Gly Trp Leu Phe Arg Ala Ile Pro Ala Ser Val Glu His Gly Arg Val
115 120 125
Tyr Val Gly Asn Val Ala Trp Met His Val Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140
Xaa Xaa Xaa Xaa Xaa Xaa Met Gly Gly Val Tyr Phe Cys Tyr Asp Gly
145 150 155 160
Ser Pro Tyr Arg Ser Tyr Glu Asp Phe Asn Met Glu Phe Leu Gly Pro
165 170 175
Cys Gly Leu Arg Leu Val Gly Ala Arg Pro Leu Leu Pro Tyr Trp Xaa
180 185 190
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
195 200 205
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Pro Tyr Thr Leu Ala Val
210 215 220
Ala Asn Thr Thr Phe Thr Val Ser Thr Asp Lys Ala Gln Arg His Phe
225 230 235 240
Gly Tyr Glu Pro Leu Phe Ser Trp Glu Asp Ser Arg Thr Arg Thr Ile
245 250 255
Leu Trp Val Gln
260

<210> 26
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-beta hydroxysteroid dehydrogenase delta5 domain

<400> 26
Val Tyr Leu Val Thr Gly Gly Cys Gly Phe Leu Gly Glu His Val Val

1 5 10 15
 Arg Met Leu Leu Gln Arg Glu
 20

<210> 27
 <211> 35
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> short chain dehydrogenase/reductase C2 domain

<400> 27
 Gly Arg Leu Gly Glu Pro Glu Glu Ile Ala Asn Ala Val Val Phe Leu
 1 5 10 15
 Ala Ser Asp Ala Ala Ser Asp Ala Ala Ser Tyr Ile Thr Gly Gln Thr
 20 25 30
 Leu Val Val
 35

<210> 28
 <211> 181
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> oxidoreductase protein dehydrogenase NAD reductase
 domain

<400> 28
 Lys Ala Ile Val Lys Glu Leu Leu Glu Leu Gly Ser Asn Val Val Ile
 1 5 10 15
 Ala Lys Arg Lys Leu Glu Arg Leu Lys Ser Ala Ala Asp Glu Leu Gln
 20 25 30
 Ala Asn Leu Pro Pro Thr Lys Gln Ala Arg Val Ile Pro Ile Gln Cys
 35 40 45
 Asn Ile Arg Asn Glu Glu Glu Val Asn Asn Leu Val Lys Ser Thr Leu
 50 55 60
 Asp Thr Phe Gly Lys Ile Asn Phe Leu Cys Asn Asn Gly Gly Gly Gln
 65 70 75 80
 Phe Leu Ser Pro Ala Glu His Ile Ser Ser Lys Gly Trp His Ala Val
 85 90 95
 Leu Glu Thr Asn Leu Thr Gly Thr Phe Tyr Met Cys Lys Ala Val Tyr
 100 105 110
 Ser Ser Trp Met Lys Glu His Gly Gly Ser Ile Val Asn Ile Ile Val
 115 120 125
 Pro Thr Lys Ala Gly Phe Pro Leu Ala Val His Ser Gly Ala Ala Arg
 130 135 140
 Ala Gly Val Tyr Asn Leu Thr Lys Ser Leu Ala Leu Glu Trp Ala Cys
 145 150 155 160
 Ser Gly Ile Arg Ile Asn Cys Val Ala Pro Gly Val Ile Tyr Ser Gln
 165 170 175
 Thr Ala Val Glu Asn
 180

<210> 29
 <211> 85

<212> PRT
<213> Artificial Sequence

<220>
<223> oxidoreductase protein dehydrogenase NAD reductase
domain

<400> 29
Gly Gln Val Ala Ile Val Thr Gly Gly Ala Thr Gly Ile Gly Lys Ala
1 5 10 15
Ile Val Lys Glu Leu Leu Glu Leu Gly Ser Asn Val Val Ile Ala Ser
20 25 30
Arg Lys Leu Glu Arg Leu Lys Ser Ala Ala Asp Glu Leu Gln Ala Asn
35 40 45
Leu Pro Pro Thr Lys Gln Ala Arg Val Ile Pro Ile Gln Cys Asn Ile
50 55 60
Arg Asn Glu Glu Glu Val Asn Asn Leu Val Lys Ser Thr Leu Asp Thr
65 70 75 80
Phe Gly Lys Ile Asn
85

<210> 30
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> oxidoreductase protein dehydrogenase NAD reductase
domain

<400> 30
Ala Leu Glu Trp Ala Cys Ser Gly Ile Arg Ile Asn Cys Val Ala Pro
1 5 10 15
Gly Val Ile Tyr Ser Gln Thr
20

<210> 31
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> glucose-1 dehydrogenase domain

<400> 31
Ser Phe Gln Lys Ile Pro Ala Lys Arg Ile Gly Val Pro Glu Glu Val
1 5 10 15
Ser Ser Val Val Cys Phe Leu Leu Ser Pro Ala Ala Ser Phe Ile Thr
20 25 30
Gly Gln Ser Cys Asp Cys Asp Gly Gly Arg Ser Leu Tyr
35 40 45

<210> 32
<211> 48
<212> PRT

<213> Artificial Sequence

<220>

<223> shikimate 5-dehydrogenase domain

<400> 32

Leu	Gln	Gly	Gln	Val	Ala	Ile	Val	Thr	Gly	Gly	Ala	Thr	Gly	Ile	Gly
1			5					10					15		
Lys	Ala	Ile	Val	Lys	Glu	Leu	Leu	Glu	Leu	Gly	Ser	Asn	Val	Val	Ile
		20					25					30			
Ala	Ser	Arg	Lys	Leu	Glu	Arg	Leu	Lys	Ser	Ala	Ala	Asp	Glu	Leu	Gln
	35						40					45			

<210> 33

<211> 50

<212> PRT

<213> Artificial Sequence

<220>

<223> dehydrogenase domain

<400> 33

Gln	Ser	Phe	Phe	Glu	Gly	Ser	Phe	Gln	Lys	Ile	Pro	Ala	Lys	Arg	Ile
1			5					10					15		
Gly	Val	Pro	Glu	Glu	Val	Ser	Ser	Val	Val	Cys	Phe	Leu	Leu	Ser	Pro
		20					25					30			
Ala	Ala	Ser	Phe	Ile	Thr	Gly	Gln	Ser	Val	Asp	Val	Asp	Gly	Gly	Arg
		35					40					45			
Ser	Leu														
	50														

<210> 34

<211> 52

<212> PRT

<213> Artificial Sequence

<220>

<223> hypothetical protein domain

<400> 34

Tyr	Leu	Ala	Pro	Gly	Gln	Gly	Gln	Val	Ala	Ile	Val	Thr	Gly	Gly	Ala
1			5					10					15		
Thr	Gly	Ile	Gly	Lys	Ala	Ile	Val	Lys	Glu	Leu	Leu	Glu	Leu	Gly	Ser
		20					25					30			
Asn	Val	Val	Ile	Ala	Ser	Arg	Lys	Leu	Glu	Arg	Leu	Lys	Ser	Ala	Ala
		35					40					45			
Asp	Glu	Leu	Gln												
	50														